

Differences in MicroRNA Expression Profiles of Adrenocortical Tumors – Letter

In their elegant study published in the December 15, 2009 issue of *Clinical Cancer Research*, Soon and colleagues described differences in the microRNA expression profiles of adrenocortical tumors (ACT) and established predictors for poor prognosis. Twenty-three microRNAs were found to be significantly differentially expressed between adrenocortical adenomas (ACA) and carcinomas (ACC) but only two between normal adrenal cortices (NA) and ACTs by microarray analysis. Four microRNAs were validated by quantitative real-time PCR (1).

In our previous study published in the September 2009 issue of *Endocrine-Related Cancer* (epub 22 June; ref. 2), we have performed an integrative bioinformatic analysis on ACTs including parallel microRNA (Taqman TLDA Panel) and mRNA profiling and pathway analysis. We have found 22 microRNAs with significant differences in expression among NA, hormonally inactive ACA, cortisol-producing ACA, and ACC. Six microRNAs were validated by quantitative real-time PCR. $dCT_{miR-511} - dCT_{miR-503}$ (dCT , delta cycle threshold) was identified as the best predictor of malignancy.

Whereas the number of significantly differentially expressed microRNAs was highly similar in the two studies, only two were common in both: miR-503 and miR-181b (both overexpressed in ACCs).

There are several differences between the structures of the two studies that might have accounted for these discrepancies. Although the number of tumors included in the study by Soon et al. was higher (27 ACA and 22 ACC) than in ours (19 ACA and 7 ACC), the groups have not been subdivided based on hormone secretion in the former. We have studied only cortisol-secreting ACCs, and ACAs have been subdivided into inactive ACA ($n = 10$) and cortisol-producing ACA ($n = 9$) groups. Both ACAs and ACCs express glucocorticoid receptors that are even overexpressed in ACCs (3). Adrenocortical microRNA expression patterns might be influenced by glucocorticoids.¹ This might argue against the establishment of tumor groups irrespective of their hormonal activity.

¹ A. Patócs, Z. Tömböl, P.M. Szabó, P. Igaz, K. Rácz, unpublished results.

Furthermore, we have studied intact NA ($n = 10$) removed from patients operated for malignant kidney tumors, whereas Soon et al. used NA samples ($n = 6$) from adrenalectomy specimens away from the site of the adenoma. He et al. reported that the overexpression of miR-221 characteristic for papillary thyroid cancer can be detected in the unaffected, histologically normal tissue surrounding the tumor (4). It is possible that a similar phenomenon might also exist in ACTs, and this could be related to the finding that only two microRNAs were significantly differentially expressed between NA and tumors.

Further studies will be necessary to clarify the relevance and potential diagnostic applicability of microRNAs for adrenocortical tumors.

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Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

References

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